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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/731,657
DATE: 11/29/2001
TIME: 15:35:50

Input Set : A:\09731657.raw.txt
Output Set: N:\CRF3\11292001\I731657.raw

ENTERED

SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: OSTERHOFF, CAROLINE
6 IVELL, RICHARD
8 (ii) TITLE OF INVENTION: EPIDIDYMIS-SPECIFIC RECEPTOR PROTEIN
10 (iii) NUMBER OF SEQUENCES: 11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: NIXON & VANDERHYE P.C.
14 (B) STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
15 (C) CITY: ARLINGTON
16 (D) STATE: VA
17 (E) COUNTRY: USA
18 (F) ZIP: 22201
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26 (vi) CURRENT APPLICATION DATA:
C--> 27 (A) APPLICATION NUMBER: US/09/731,657
C--> 28 (B) FILING DATE: 12-Mar-2001
29 (C) CLASSIFICATION:
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: US/09/041,745
33 (B) FILING DATE:
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: SADOFF, B.J.
37 (B) REGISTRATION NUMBER: 36,663
38 (C) REFERENCE/DOCKET NUMBER: 35-125
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: 703-816-4000
42 (B) TELEFAX: 703-816-4100
45 (2) INFORMATION FOR SEQ ID NO: 1:
47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 4665 base pairs
49 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
51 (D) TOPOLOGY: linear
53 (ii) MOLECULE TYPE: cdna
55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 1..3114
59 (ix) FEATURE:
60 (A) NAME/KEY: 3'UTR
61 (B) LOCATION: 3115..4665
63 (ix) FEATURE:
64 (A) NAME/KEY: polyA-site

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65          (B) LOCATION: 4647..4652
66          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 AGC CAG CCC GAG GAC GCG AGC GGC AGG TGT GCA CAG AGG TTC TCC ACT      48
71 Ser Gln Pro Glu Asp Ala Ser Gly Arg Cys Ala Gln Arg Phe Ser Thr
72 1          5          10          15
74 TTG TTT TCT GAA CTC GCG GTC AGG ATG GTT TTC TCT GTC AGG CAG TGT      96
75 Leu Phe Ser Glu Leu Ala Val Arg Met Val Phe Ser Val Arg Gln Cys
76          20          25          30
78 GGC CAT GTT GGC AGA ACT GAA GAA GTT TTA CTG ACG TTC AAG ATA TTC      144
79 Gly His Val Gly Arg Thr Glu Glu Val Leu Leu Thr Phe Lys Ile Phe
80          35          40          45
82 CTT GTC ATC ATT TGT CTT CAT GTC GTT CTG GTA ACA TCC CTG GAA GAA      192
83 Leu Val Ile Ile Cys Leu His Val Val Leu Val Thr Ser Leu Glu Glu
84          50          55          60
86 GAT ACT GAT AAT TCC AGT TTG TCA CCA CCA CCT GCT AAA TTA TCT GTT      240
87 Asp Thr Asp Asn Ser Ser Leu Ser Pro Pro Pro Ala Lys Leu Ser Val
88 65          70          75          80
90 GTC AGT TTT GCC CCC TCC TCC AAT GAG GTT GAA ACA ACA AGC CTC AAT      288
91 Val Ser Phe Ala Pro Ser Ser Asn Glu Val Glu Thr Thr Ser Leu Asn
92          85          90          95
94 GAT GTT ACT TTA AGC TTA CTC CCT TCA AAC GAA ACA GAA AAA ACT AAA      336
95 Asp Val Thr Leu Ser Leu Leu Pro Ser Asn Glu Thr Glu Lys Thr Lys
96          100          105          110
98 ATC ACT ATA GTA AAA ACC TTC AAT GCT TCA GGC GTC AAA CCC CAG AGA      384
99 Ile Thr Ile Val Lys Thr Phe Asn Ala Ser Gly Val Lys Pro Gln Arg
100          115          120          125
102 AAT ATC TGC AAT TTG TCA TCT ATT TGC AAT GAC TCA GCA TTT TTT AGA      432
103 Asn Ile Cys Asn Leu Ser Ser Ile Cys Asn Asp Ser Ala Phe Phe Arg
104          130          135          140
106 GGT GAG ATC ATG TTT CAA TAT GAT AAA GAA AGC ACT GTT CCC CAG AAT      480
107 Gly Glu Ile Met Phe Gln Tyr Asp Lys Glu Ser Thr Val Pro Gln Asn
108 145          150          155          160
110 CAA CAT ATA ACG AAT GGC ACC TTA ACT GGA GTC CTG TCT CTA AGT GAA      528
111 Gln His Ile Thr Asn Gly Thr Leu Thr Gly Val Leu Ser Leu Ser Glu
112          165          170          175
114 TTA AAA CGC TCA GAG CTC AAC AAA ACC CTG CAA ACC CTA AGT GAG ACT      576
115 Leu Lys Arg Ser Glu Leu Asn Lys Thr Leu Gln Thr Leu Ser Glu Thr
116          180          185          190
118 TAC TTT ATA ATG TGT GCT ACA GCA GAG GCC CAA AGC ACA TTA AAT TGT      624
119 Tyr Phe Ile Met Cys Ala Thr Ala Glu Ala Gln Ser Thr Leu Asn Cys
120          195          200          205
122 ACA TTC ACA ATA AAA CTG AAT AAT ACA ATG AAT GCA TGT GCT GCA ATA      672
123 Thr Phe Thr Ile Lys Leu Asn Asn Thr Met Asn Ala Cys Ala Ala Ile
124          210          215          220
126 GCC GCT TTG GAA AGA GTA AAG ATT CGA CCA ATG GAA CAC TGC TGC TGT      720
127 Ala Ala Leu Glu Arg Val Lys Ile Arg Pro Met Glu His Cys Cys Cys
128 225          230          235          240
130 TCT GTC AGG ATA CCC TGC CCT TCC TCC CCA GAA GAG TTG GGA AAG CTT      768
131 Ser Val Arg Ile Pro Cys Pro Ser Ser Pro Glu Glu Leu Gly Lys Leu

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132		245		250		255	
134	CAG TGT GAC CTG CAG GAT CCC ATT GTC TGT CTT GCT GAC CAT CCA CGT						816
135	Gln Cys Asp Leu Gln Asp Pro Ile Val Cys Leu Ala Asp His Pro Arg						
136		260		265		270	
138	GGC CCA CCA TTT TCT TCC AGC CAA TCC ATC CCA GTG GTG CCT CGG GCC						864
139	Gly Pro Pro Phe Ser Ser Ser Gln Ser Ile Pro Val Val Pro Arg Ala						
140		275		280		285	
142	ACT GTG CTT TCC CAG GTC CCC AAA GCT ACC TCT TTT GCT GAG CCT CCA						912
143	Thr Val Leu Ser Gln Val Pro Lys Ala Thr Ser Phe Ala Glu Pro Pro						
144		290		295		300	
146	GAT TAT TCA CCT GTG ACC CAC AAT GTT CCC TCT CCA ATA GGG GAG ATT						960
147	Asp Tyr Ser Pro Val Thr His Asn Val Pro Ser Pro Ile Gly Glu Ile						
148	305		310		315	320	
150	CAA CCC CTT TCA CCC CAG CCT TCA GCT CCC ATA GCT TCC AGC CCT GCC						1008
151	Gln Pro Leu Ser Pro Gln Pro Ser Ala Pro Ile Ala Ser Ser Pro Ala						
152		325		330		335	
154	ATT GAC ATG CCC CCA CAG TCT GAA ACG ATC TCT TCC CCT ATG CCC CAA						1056
155	Ile Asp Met Pro Pro Gln Ser Glu Thr Ile Ser Ser Pro Met Pro Gln						
156		340		345		350	
158	ACC CAT GTC TCC GGC ACC CCA CCT CCT GTG AAA GCC TCA TTT TCC TCT						1104
159	Thr His Val Ser Gly Thr Pro Pro Pro Val Lys Ala Ser Phe Ser Ser						
160		355		360		365	
162	CCC ACC GTG TCT GCC CCT GCG AAT GTC AAC ACT ACC AGC GCA CCT CCT						1152
163	Pro Thr Val Ser Ala Pro Ala Asn Val Asn Thr Thr Ser Ala Pro Pro						
164		370		375		380	
166	GTC CAG ACA GAC ATC GTC AAC ACC AGC AGT ATT TCT GAT CTT GAG AAC						1200
167	Val Gln Thr Asp Ile Val Asn Thr Ser Ser Ile Ser Asp Leu Glu Asn						
168	385		390		395	400	
170	CAA GTG TTG CAG ATG GAG AAG GCT CTG TCC TTG GGC AGC CTG GAG CCT						1248
171	Gln Val Leu Gln Met Glu Lys Ala Leu Ser Leu Gly Ser Leu Glu Pro						
172		405		410		415	
174	AAC CTC GCA GGA GAA ATG ATC AAC CAA GTC AGC AGA CTC CTT CAT TCC						1296
175	Asn Leu Ala Gly Glu Met Ile Asn Gln Val Ser Arg Leu Leu His Ser						
176		420		425		430	
178	CCG CCT GAC ATG CTG GCC CCT CTG GCT CAA AGA TTG CTG AAA GTA GTG						1344
179	Pro Pro Asp Met Leu Ala Pro Leu Ala Gln Arg Leu Leu Lys Val Val						
180		435		440		445	
182	GAT GAC ATT GGC CTA CAG CTG AAC TTT TCA AAC ACG ACT ATA AGT CTA						1392
183	Asp Asp Ile Gly Leu Gln Leu Asn Phe Ser Asn Thr Thr Ile Ser Leu						
184		450		455		460	
186	ACC TCC CCT TCT TTG GCT CTG GCT GTG ATC AGA GTG AAT GCC AGT AGT						1440
187	Thr Ser Pro Ser Leu Ala Leu Ala Val Ile Arg Val Asn Ala Ser Ser						
188	465		470		475	480	
190	TTC AAC ACA ACT ACC TTT GTG GCC CAA GAC CCT GCA AAT CTT CAG GTT						1488
191	Phe Asn Thr Thr Thr Phe Val Ala Gln Asp Pro Ala Asn Leu Gln Val						
192		485		490		495	
194	TCT CTG GAA ACC CAA GCT CCT GAG AAC AGT ATT GGC ACA ATT ACT CTT						1536
195	Ser Leu Glu Thr Gln Ala Pro Glu Asn Ser Ile Gly Thr Ile Thr Leu						
196		500		505		510	

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198	CCT	TCA	TCG	CTG	ATG	AAT	AAT	TTA	CCA	GCT	CAT	GAC	ATG	GAG	CTA	GCT	1584
199	Pro	Ser	Ser	Leu	Met	Asn	Asn	Leu	Pro	Ala	His	Asp	Met	Glu	Leu	Ala	
200			515					520					525				
202	TCC	AGG	GTT	CAG	TTC	AAT	TTT	TTT	GAA	ACA	CCT	GCT	TTG	TTT	CAG	GAT	1632
203	Ser	Arg	Val	Gln	Phe	Asn	Phe	Phe	Glu	Thr	Pro	Ala	Leu	Phe	Gln	Asp	
204			530				535					540					
206	CCT	TCC	CTG	GAG	AAC	CTC	TCT	CTG	ATC	AGC	TAC	GTC	ATA	TCA	TCG	AGT	1680
207	Pro	Ser	Leu	Glu	Asn	Leu	Ser	Leu	Ile	Ser	Tyr	Val	Ile	Ser	Ser	Ser	
208			545			550					555					560	
210	GTT	GCA	AAC	CTG	ACC	GTC	AGG	AAC	TTG	ACA	AGA	AAC	GTG	ACA	GTC	ACA	1728
211	Val	Ala	Asn	Leu	Thr	Val	Arg	Asn	Leu	Thr	Arg	Asn	Val	Thr	Val	Thr	
212				565						570					575		
214	TTA	AAG	CAC	ATC	AAC	CCG	AGC	CAG	GAT	GAG	TTA	ACA	GTG	AGA	TGT	GTA	1776
215	Leu	Lys	His	Ile	Asn	Pro	Ser	Gln	Asp	Glu	Leu	Thr	Val	Arg	Cys	Val	
216			580					585					590				
218	TTT	TGG	GAC	TTG	GGC	AGA	AAT	GGT	GGC	AGA	GGA	GGC	TGG	TCA	GAC	AAT	1824
219	Phe	Trp	Asp	Leu	Gly	Arg	Asn	Gly	Gly	Arg	Gly	Gly	Trp	Ser	Asp	Asn	
220			595				600					605					
222	GGC	TGC	TCT	GTC	AAA	GAC	AGG	AGA	TTG	AAT	GAA	ACC	ATC	TGT	ACC	TGT	1872
223	Gly	Cys	Ser	Val	Lys	Asp	Arg	Arg	Leu	Asn	Glu	Thr	Ile	Cys	Thr	Cys	
224			610			615					620						
226	AGC	CAT	CTA	ACA	AGC	TTC	GGC	GTT	CTG	CTG	GAC	CTA	TCT	AGG	ACA	TCT	1920
227	Ser	His	Leu	Thr	Ser	Phe	Gly	Val	Leu	Leu	Asp	Leu	Ser	Arg	Thr	Ser	
228			625			630				635					640		
230	GTG	CTG	CCT	GCT	CAA	ATG	ATG	GCT	CTG	ACG	TTC	ATT	ACA	TAT	ATT	GGT	1968
231	Val	Leu	Pro	Ala	Gln	Met	Met	Ala	Leu	Thr	Phe	Ile	Thr	Tyr	Ile	Gly	
232				645						650					655		
234	TGT	GGG	CTT	TCA	TCA	ATT	TTT	CTG	TCA	GTG	ACT	CTT	GTA	ACC	TAC	ATA	2016
235	Cys	Gly	Leu	Ser	Ser	Ile	Phe	Leu	Ser	Val	Thr	Leu	Val	Thr	Tyr	Ile	
236			660					665					670				
238	GCT	TTT	GAA	AAG	ATC	CGG	AGG	GAT	TAC	CCT	TCC	AAA	ATC	CTC	ATC	CAG	2064
239	Ala	Phe	Glu	Lys	Ile	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu	Ile	Gln	
240			675					680					685				
242	CTG	TGT	GCT	GCT	CTG	CTT	CTG	CTG	AAC	CTG	GTC	TTC	CTC	CTG	GAC	TCG	2112
243	Leu	Cys	Ala	Ala	Leu	Leu	Leu	Leu	Asn	Leu	Val	Phe	Leu	Leu	Asp	Ser	
244			690			695					700						
246	TGG	ATT	GCT	CTG	TAT	AAG	ATG	CAA	GGC	CTC	TGC	ATC	TCA	GTG	GCT	GTA	2160
247	Trp	Ile	Ala	Leu	Tyr	Lys	Met	Gln	Gly	Leu	Cys	Ile	Ser	Val	Ala	Val	
248			705			710				715					720		
250	TTT	CTT	CAT	TAT	TTT	CTC	TTG	GTC	TCA	TTC	ACA	TGG	ATG	GGC	CTA	GAA	2208
251	Phe	Leu	His	Tyr	Phe	Leu	Leu	Val	Ser	Phe	Thr	Trp	Met	Gly	Leu	Glu	
252				725					730				735				
254	GCA	TTC	CAT	ATG	TAC	CTG	GCC	CTT	GTC	AAA	GTA	TTT	AAT	ACT	TAC	ATC	2256
255	Ala	Phe	His	Met	Tyr	Leu	Ala	Leu	Val	Lys	Val	Phe	Asn	Thr	Tyr	Ile	
256			740					745					750				
258	CGA	AAA	TAC	ATC	CTT	AAA	TTC	TGC	ATT	GTC	GGT	TGG	GGG	GTA	CCA	GCT	2304
259	Arg	Lys	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Val	Gly	Trp	Gly	Val	Pro	Ala	
260			755					760					765				
262	GTG	GTT	GTG	ACC	ATC	ATC	CTG	ACT	ATA	TCC	CCA	GAT	AAC	TAT	GGG	CTT	2352

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263	Val	Val	Val	Thr	Ile	Ile	Leu	Thr	Ile	Ser	Pro	Asp	Asn	Tyr	Gly	Leu	
264		770					775					780					
266	GGA	TCC	TAT	GGG	AAA	TTC	CCC	AAT	GGT	TCA	CCG	GAT	GAC	TTC	TGC	TGG	2400
267	Gly	Ser	Tyr	Gly	Lys	Phe	Pro	Asn	Gly	Ser	Pro	Asp	Asp	Phe	Cys	Trp	
268	785					790					795					800	
270	ATC	AAC	AAC	AAT	GCA	GTA	TTC	TAC	ATT	ACG	GTG	GTG	GGA	TAT	TTC	TGT	2448
271	Ile	Asn	Asn	Asn	Ala	Val	Phe	Tyr	Ile	Thr	Val	Val	Gly	Tyr	Phe	Cys	
272					805					810						815	
274	GTG	ATA	TTT	TTG	CTG	AAC	GTC	AGC	ATG	TTC	ATT	GTG	GTC	CTG	GTT	CAG	2496
275	Val	Ile	Phe	Leu	Leu	Asn	Val	Ser	Met	Phe	Ile	Val	Val	Leu	Val	Gln	
276				820					825					830			
278	CTC	TGT	CGA	ATT	AAA	AAG	AAG	AAG	CAA	CTG	GGA	GCC	CAG	CGA	AAA	ACC	2544
279	Leu	Cys	Arg	Ile	Lys	Lys	Lys	Lys	Gln	Leu	Gly	Ala	Gln	Arg	Lys	Thr	
280			835						840					845			
282	AGT	ATT	CAA	GAC	CTC	AGG	AGT	ATC	GCT	GGC	CTT	ACA	TTT	TTA	CTG	GGA	2592
283	Ser	Ile	Gln	Asp	Leu	Arg	Ser	Ile	Ala	Gly	Leu	Thr	Phe	Leu	Leu	Gly	
284		850				855						860					
286	ATA	ACT	TGG	GGC	TTT	GCC	TTC	TTT	GCC	TGG	GGA	CCA	GTT	AAC	GTG	ACC	2640
287	Ile	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Val	Asn	Val	Thr	
288	865				870					875						880	
290	TTC	ATG	TAT	CTG	TTT	GCC	ATC	TTT	AAT	ACC	TTA	CAA	GGA	TTT	TTC	ATA	2688
291	Phe	Met	Tyr	Leu	Phe	Ala	Ile	Phe	Asn	Thr	Leu	Gln	Gly	Phe	Phe	Ile	
292				885						890						895	
294	TTC	ATC	TTT	TAC	TGT	GTG	GCC	AAA	GAA	AAT	GTC	AGG	AAG	CAA	TGG	AGG	2736
295	Phe	Ile	Phe	Tyr	Cys	Val	Ala	Lys	Glu	Asn	Val	Arg	Lys	Gln	Trp	Arg	
296				900					905					910			
298	CGG	TAT	CTT	TGT	TGT	GGA	AAG	TTA	CGG	CTG	GCT	GAA	AAT	TCT	GAC	TGG	2784
299	Arg	Tyr	Leu	Cys	Cys	Gly	Lys	Leu	Arg	Leu	Ala	Glu	Asn	Ser	Asp	Trp	
300			915					920						925			
302	AGT	AAA	ACT	GCT	ACT	AAT	GGT	TTA	AAG	AAG	CAG	ACT	GTA	AAC	CAA	GGA	2832
303	Ser	Lys	Thr	Ala	Thr	Asn	Gly	Leu	Lys	Lys	Gln	Thr	Val	Asn	Gln	Gly	
304		930				935					940						
306	GTG	TCC	AGC	TCT	TCA	AAT	TCC	TTA	CAG	TCA	AGC	AGT	AAC	TCC	ACT	AAC	2880
307	Val	Ser	Ser	Ser	Ser	Asn	Ser	Leu	Gln	Ser	Ser	Ser	Asn	Ser	Thr	Asn	
308	945				950					955						960	
310	TCC	ACC	ACA	CTG	CTA	GTG	AAT	AAT	GAT	TGC	TCA	GTA	CAC	GCA	AGC	GGG	2928
311	Ser	Thr	Thr	Leu	Leu	Val	Asn	Asn	Asp	Cys	Ser	Val	His	Ala	Ser	Gly	
312				965						970						975	
314	AAT	GGA	AAT	GCT	TCT	ACA	GAG	AGG	AAT	GGG	GTC	TCT	TTT	AGT	GTT	CAG	2976
315	Asn	Gly	Asn	Ala	Ser	Thr	Glu	Arg	Asn	Gly	Val	Ser	Phe	Ser	Val	Gln	
316			980					985						990			
318	AAT	GGA	GAT	GTG	TGC	CTT	CAC	GAT	TTC	ACT	GGA	AAA	CAG	CAC	ATG	TTT	3024
319	Asn	Gly	Asp	Val	Cys	Leu	His	Asp	Phe	Thr	Gly	Lys	Gln	His	Met	Phe	
320			995					1000						1005			
322	AAC	GAG	AAG	GAA	GAT	TCC	TGC	AAT	GGG	AAA	GGC	CGT	ATG	GCT	CTC	AGA	3072
323	Asn	Glu	Lys	Glu	Asp	Ser	Cys	Asn	Gly	Lys	Gly	Arg	Met	Ala	Leu	Arg	
324		1010				1015					1020						
326	AGG	ACT	TCA	AAG	CGG	GGA	AGC	TTA	CAC	TTT	ATT	GAG	CAA	ATG			3114
327	Arg	Thr	Ser	Lys	Arg	Gly	Ser	Leu	His	Phe	Ile	Glu	Gln	Met			

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11